IN THE CLAIMS

The following listing of claims replaces all prior versions, and listings, of claims in this application:

Claims 1-22 (Cancelled)

23. (New) A process for fermentatively preparing an L-amino acid, comprising

fermenting a modified microorganism of the *Enterobacteriaceae* family for a time and under conditions suitable for the production of the L-amino acid; and

isolating the L-amino acid,

wherein said modified microorganism comprises an attenuated poxB gene which encodes a pyruvate oxidase.

24. (New) The process of Claim 23, further comprising concentrating the L-amino acid in a medium used for the fermenting or in cells of the modified microorganism prior to isolating the L-amino acid.

25. (New) The process of Claim 23, wherein said L-amino acid is L-threonine, L-valine, L-lysine, L-isoleucine, L-methionine, or L-homoserine.

26. (New) The process of Claim 25, wherein said L-amino acid is L-threonine.

27. (New) The process of Claim 25, wherein said L-amino acid is L-valine.

28. (New) The process of Claim 25, wherein said L-amino acid is L-lysine.

29. (New) The process of Claim 23, wherein the poxB gene product is not expressed.

30. (New) The process of Claim 23, wherein the modified microorganism further comprises at least one overexpressed gene product compared to the unmodified starting microorganism, wherein the gene product is encoded by a gene selected from the group consisting of:

at least one gene encoded by thrABC operon, which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase, and threonine synthase,

a *Corynebacteriumm glutamicum* pyc gene which codes for pyruvate carboxylase,

pps gene which codes for phosphoenol pyruvate synthase,

ppc gene which codes for phosphoenol pyruvate carboxylase,

pntA and pntB genes which code for pyridine transhydrogenase,

an *Escherichia coli* rhtB gene which imparts homoserine resistance,

mqo gene which codes for malate:quinone oxidoreductase,

an *Escherichia coli* rhtC gene which imparts threonine resistance,

an *Corynebacterium glutamicum* thrE gene which codes for threonine export, and

gdhA gene which codes for glutamate dehydrogenase.

31. (New) The process of Claim 23, wherein the modified microorganism further comprises at least one gene whose expression is reduced or eliminated compared to the unmodified starting microorganism, wherein the at least one gene is selected from the group consisting of tdh gene which codes for threonine dehydrogenase, mdh gene which codes for malate dehydrogenase, and pckA gene which codes for the enzyme phosphoenol pyruvate carboxykinase.

32. (New) The process of Claim 31, wherein the at least one gene is eliminated.

33. (New) The process of Claim 23, wherein the modified microorganism is *Escherichia coli*.

34. (New) The process of Claim 33, wherein the modified microorganism further comprises at least one gene whose expression is eliminated compared to the unmodified starting microorganism, wherein the at least one gene is an *E. coli* yjfA or ytfP.

35. (New) The process of Claim 26, wherein the modified microorganism is MG442ΔpoxB transformed with plasmid pMW218gdhA.

36.(New) The process of Claim 26, wherein the modified microorganism is MG442ΔpoxB transformed with plasmid pMW219rhtC.

37. (New) The process of Claim 28, wherein the modified microorganism is TOC21RΔpoxB.

38. (New) The process of Claim 27, wherein the modified microorganism is B-12288ΔpoxB.